

**ABSTRACT**

Methods of identifying molecular interaction sites in eukaryotic and prokaryotic nucleic acids, especially RNA, are described. Secondary structural elements are identified from highly conserved sequences. Methods of preparing databases relating to such molecular interaction sites are also provided herein as are databases themselves. Therapeutic, agricultural, industrial, and other applicability results from interaction of such molecular interaction sites with "small" and other molecules.

09310567-051299  
662750-990760